AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

- 1.-19. (Canceled).
- 20. (Currently amended) A method for identifying a candidate protein useful as an anti-infective, comprising:
- (a) calculating computationally protein sequence-based attributes from all protein sequences of a pathogenic organism, wherein said protein sequence-based attributes are selected from a group consisting of percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity, and measure of hydrophobicity from a fixed reference frame;
- (b) clustering computationally said all protein sequences based on said protein sequencebased attributes using Principle Component Analysis;
- (c) identifying computationally outlier proteins, wherein said outlier proteins appear outside a main cluster;
- (d) comparing said outlier proteins to known proteins to identify a unique outlier protein; and
 - (e)(d) validating said-unique outlier protein as an anti-infective.
- 21. (Previously presented) The method of claim 20, wherein said pathogenic organism is selected from the group consisting of *B.burgdorfei*, *C.jejuni*, *C.pneumoniae*, *C.trachomatis*,

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H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae.

- 22. (Previously presented) The method of claim 20, wherein said protein sequence-based attributes are selected from the group consisting of fixed protein attributes and variable protein attributes.
- 23. (**Previously presented**) The method of claim 22, wherein a variable protein attribute is a distance of protein sequence from a variable reference frame.
- 24. (Previously presented) The method of claim 20, wherein said clustering is done by Principle Component Analysis using correlation coefficient between said protein sequence-based attributes.
- 25. (Previously presented) The method of claim 20, wherein said clustering is based upon analysis of protein sequence-based attributes and not based upon sequence pattern linked to biochemical functions.
- 26. (Currently amended) The method of claim 20, wherein said-unique outlier protein is non-homologous to known anti-infective proteins from a pathogen selected from the group consisting of B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae.

- 27. (Currently amended) The method of claim 20, wherein said-unique outlier protein has an amino acid sequence selected from the group consisting of SEQ ID Nos: 1-31.
- 28. (Currently amended) The method of claim 20, wherein said-unique outlier protein has an amino acid sequence selected from the group consisting of SEQ ID Nos: 32-118.
- 29. (**Previously presented**) The method of claim 20, wherein steps are performed by a computer system comprising:
- (1) a central processing unit (CPU), wherein said CPU executes DISTANCE program and clusters protein sequences based on protein sequence-based attributes using Principle Component Analysis, thereby producing results;
 - (2) a memory device accessed by said CPU, wherein said memory device stores said results;
 - (3) a display on which said CPU displays said results in response to user inputs; and
 - (4) a user interface device.
- 30. (Currently amended) The method of claim 20, wherein said-unique outlier protein may be used for a diagnostic purpose.
 - 31. (Canceled)

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- 32. (Currently amended) The method of claim 20, wherein said-unique outlier protein may be used for a therapeutic purpose.
- 33. (Currently amended) The method as of claim 20, wherein said-unique outlier protein can elicit an immune response.